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ALIGNMENTS

RESULT 1 ADD84537

ADD84537;

ADD84537 standard; protein; 205 AA.

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The present invention describes a composition (I) comprising a substance that modulates the status of 121PIFI (gene and encoded protein), or a molecule that is modulated by 121PIFI, where the status of a cell that expresses 121PIFI is modulated. The human 121PIFI gene maps to chromosome 4q. (I) has cycostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121PIFI, such as breast, colon, ovarian or lung cancer. The 121PIFI gene or its
                                                                                                                                                                                                   Composition comprising a substance that modulates the status of 121P1F1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or
                                                                                                                                                      Claim 19; Fig 2A; 285pp; English.
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N-PSDB; ADD84536.
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fragment can be used to elicit a humoral or cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarchritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                           Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correl with the disease.
                                                                                                                                                                                                                                                                                                                                                                              12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-2003; 2003WO-US010870.
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                        English.
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CC for therapeutic intervention in treating a disease associated with CC altered mitochondrial function. Specifically, it refers to a method for CC identifying proteins of the human heart mitochondrial proteome that are CC useful for drug screening assays, as well as therapeutic targets. The CC present invention describes a method for identifying such proteins that CC can be used in the treatment of various diseases associated with altered CC contect in the treatment of various diseases associated with altered CC entertail function including diabetes mellitus, Huntington's disease, CC osteoarthitis, Leber's hareditary optic neuropathy (LHON), mitochondrial CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these CC compositions have neuroprotective, nootropic, antidiabetic, antiarthritic, osteopathic, ophthalmological and CC cytostatic activities. This polypeptide sequence is a human heart vice mitochondrial protein of the invention. This invention relates to novel mitochondrial targets that can be used

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JAKOBOVITS
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te antigen; prostate cancer; bladder cancer; kidney cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ng cancer; pancreatic cancer; breast cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 205
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Pred. No. 1.8e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC recombinant protein comprising an antispen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a chain monoclonal antibody, a chybridoma that produces an antibody, a single chain monoclonal antibody comprising the heavy and light chains of a monoclonal antibody comprising a polymucleotide that encodes a single chain monoclonal antibody, a polymucleotide that encodes a single chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, inhibiting growth of cancer cells that expresses composition, treating that expresses 121PFI, inhibiting growth of cancer cells that expresses composition, treating a commandation immune response directed to 121PFI, inducing an immune composition and comprise directed to 121PFI, inducing an immune composition and individual and an assay for detecting the composition may comprise a polymucleotide that comprises a lile the composition is suspected of having cancer. The composition may comprise a polymucleotide that comprises a 121PFI composition is useful that the coding sequence does not encode the entire amino acid sequence of 121PFI (ADM83793. The composition is useful for detecting the peptides being HIAA (human leukocyte antigen)-binding epitopes from 121PFI or its substance variants. The composition is useful for detecting, treating or preventing cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer. The composition can also be used as a composition to the specification). The specific sequence is a 121PFI protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 205
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Jakobovits A;
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KRKFGFEENKIDRTFGIPEDFDYID
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Pred. No. 1
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1.8e-88;
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CC modulates the status of 121PIF1 (a protein encoded by a cancer expressed CC gene) or a molecule that is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a crecombinant protein comprising an antipody a single chain monoclonal composition comprising an antipody. A single chain monoclonal comprising an antibody, a single chain monoclonal antibody, a non-human transgenic animal that produces an antibody cantibody, a vector comprising a polymucleotide that encodes a single chain monoclonal antibody, a vector comprising a polymucleotide that encodes a single comprision of comprising a cytotoxic agent or a diagnostic agent to a cell that expresses 121PIF1 (comprising a cytotoxic agent or a diagnostic agent to a cell comprising administering to the cancer cells that expresses 121PIF1 (comprising administering to the cancer cells that expresses 121PIF1 (comprising administering to the cells the composition), treating a patient who has or who is suspected to 121PIF1, inducing an immune capponse directed to 121PIF1, inducing ancer. The capponse direct who has or who is suspected of having cancer. The capponse directed to 121PIF1 (ADMSJ'93). The subject of the telestone capponse directed to 121PIF1 (ADMSJ'93). The capponse directed to 121PIF1 (ADMSJ'93). The paper direction in th
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cervical cancer
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HUBERT R S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA; human leukocyte antigen; prostate cancer; bladder cancer; kidney ca: colon cancer; lung cancer; pancreatic cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 205 AA;
                                                                         New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                             Challita-Eid PM,
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                                                        treating or preventing 
lung cancer.
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RAITANO A B.
FARIS M.
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GEW.
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                                                                                                                                                                                                                                                                                Hubert
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Pred. No. 1.8e-88;
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Disclosure; SEQ ID ĕ 211pp; English

Composition status or 121P/F1 (a protein encoded by a cancer expressed that expresses 121PIF1 is modulated. Also included are apharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121PIF1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal continuous that produces an antibody, a single chain monoclonal antibody, a vector comprising a polynucleotide that encodes an analogue continuous comprising a cytotoxic agent or a diagnostic agent to a cell comprising a cytotoxic agent or a diagnostic agent to a cell that expresses 121PIF1, inhibiting growth of cancer cells that expresses 121PIF1, inhibiting growth of cancer cells that expresses 121PIF1, inhibiting growth of cancer cells that expresses 121PIF1, an a patient who has or who is suspected of having cancer, monitoring the cresponse, monitoring 121PIF1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the composition may comprise a polynucleotide that the comprises a latest one peptide given in 16 Tables (given in the specification), the peptides of encode the entire animo acid sequence of 121PIF1 (ADM83793. The composition may comprise a polynucleotide that the coding sequence does continuous entire animo acid sequence of 121PIF1 (ADM83793. The composition acid sequence of 121PIF1 or its being HLA (human leukocyte antigen) -binding epitopes from 121PIF1 or its gentered concer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, hung cancer, pancreatic cancer, breast cancer, kidney cervical cancer or stomach cancer. The composition can also be used as a cancer for 121PIF1 is located on chromosome 4q. The present concernesses modulates the status of 121P1F1 (a progene) or a molecule that is modulated sequence is a 121P1F1 protein (full-length or fragment). invention relates to a composition comprising a substance that ulates the status of 121P1P1 (a protein encoded by a cancer exp expressed

Sequence 205 AA;

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Best Local
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KRKFGFEENKIDRTFGIPEDFDYID 205
                                                                                                                              DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
                                                                       TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
                                                                                                             DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETBER
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Pred. No. 1.8e-88;
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ADM83793

standard; protein; 205

03-JUN-2004 (first entry)

Human cancer gene 121P1F1 protein

RESULT 6
ADM83793
ID ADM8
XX
AC ADM8
XC ADM8
X Human; cancer gene 121P1F1; cytostatic; cancer; chromosome human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer; 4q; HLA;

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CC recombinant protein comprising an antispen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a single chain monoclonal antibody, a chybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121PIF1-related protein (comprising CC the variable domains of the heavy and light chains of a monoclonal antibody a vector comprising a polymucleotide that encodes a single chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue chain monoclonal antibody, a polymucleotide that encodes an analogue compises a 121PIF1, inhibiting growth of cancer cells that expresses cell 121PIF1 (comprising administering the collection of the calcs of the calcs of the cells that expresses 121PIF1, generating a commandation immune response directed to 121PIF1, inducing an immune composition may comprise a polymucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polymucleotide that comprises a 121PIF1 (comprises a polymucleotide that comprises a 121PIF1 (comprises a polymucleotide that comprises at 121PIF1 (composition), the peptides composition of the specification), the peptides comprise comprises a polymucleotide that comprises at least one composition is useful for detecting, treating or its glice variants. The composition is useful for detecting, treating or its glice variants. The composition is useful for detecting, treating or its glice variants cancer, lands be used as a carcine to treat or pervent cancer. The composition can also be used as a carcine to treat or pervent cancer that expresses or overexpresses compo
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cervical cancer; stomach cancer; gene therapy; vaccine.
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GEW.
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FARIS M.
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The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
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                                                                                                                                                                                                                                            Challita-Eid PM,
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antigen; prostate cancer; bladder cancer; kidney
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                                28-FEB-2002; 2002US-00087190.
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                                                                                  Query Match
Best Local Similarity
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                                                                                Sequence 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 14; 211pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating or preventing
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GE W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAKOBOVITS A.
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                                                                                                                          is a 121P1F1
ilarity 100.0%;
Conservative 0
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                                                                                                                          protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer e.g. prostate,
Score 1047; DB 8;
Pred. No. 1.8e-88;
; Mismatches 0;
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                                           8,
                                         Length
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RESULT 9
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ID ABP75541
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XX ABP7
XX ABP7
XX Huma

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dufour GE, Hillman JL, Yu JY, T
Daughtery SC, Dam TC, Liu TF, N
Peralta CH, David MH, Lewis SA,
Flores V, Marwaha R, Lo A, Lan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
                      The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (ABZ15837-ABZ36403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence, a polynucleotide complementary to them or an RNA equivalent of them. The polypeptide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia; asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-Inflammatory; immunosuppressive; neuroprotective; nootropic; neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipporiatic; antianaemic; anti-HIV; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                             Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                     New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2002; 2002WO-US009921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secretory polynucleotide; secretory protein.
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                                                                                                                                                                                                                                                                                                          SEQ
     neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-0280067P.

2001US-0280068P.

; 2001US-0291280P.

; 2001US-0291829P.

; 2001US-0291849P.

; 2001US-029428P.

; 2001US-0299776P.

; 2001US-0300001P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
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     disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dahl CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dahl CR, Gietzen D, Chinn J
Tuason O, Yap PE, Amshey
Nguyen DA, Kleefeld Y, Ge
Nguyen DA, Panzer SR, Haz
A, Chen AJ, Panzer SR, Haz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                          Sequence Listing; English.
     (e.g.
     epilepsy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerstin 1
Harris B;
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RESULT 10
ADM83834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. psoriasis, polycythemia vera, or cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brair breast, cervix or prostate). The present sequence is one of the SPTM proteins of the invention (ABP75384-ABP75962). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                    (CHAL/)
(HUBE/)
(RAIT/)
(FARI/)
                      WPI; 2004-060522/06
                                                                                                                                                                              08-FEB-2001; 2001US-00779250
                                                                                                                                                                                                                                                                                                  cervical cancer;
                                                                                                                                                                                                                                                                                                              human leukocyte antigen; colon cancer; lung cancer
                                                                                                                                                                                                                                                                                                                                                             Human cancer
                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                              Jakobovits
                                                        Challita-Eid PM,
                                                                                                                                                                                                      28-FEB-2002; 2002US-00087190
                                                                                                                                                                                                                                                   US2003223997-A1
                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                        (AFAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                           cancer gene 121P1F1; cytostatic; cancer; chromosome 4
leukocyte antigen; prostate cancer; bladder cancer; ki
cancer; lung cancer; pancreatic cancer; breast cancer;
                                                                                                     CHALLITA-EID P N
HUBERT R S.
RAITANO A B.
FARIS M.
AFAR D E H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                                                                            GE ₩.
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                                                                                 JAKOBOVITS A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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                                              P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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A
                                                                                                                                                                                                                                                                                                                                                             gene 121P1F1 variant protein
                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                                                                  ng cancer; pancreatic stomach cancer; gene
                                                          Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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                                                          RS,
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Pred. No. 1.9e-88;
                                                          Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                  gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
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                                                          Faris
                                                          z,
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composition comprising

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substance that modulates

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RESULT 11
ADM83835
ID ADM83
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AC ADM83
XX
DT 03-JI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition may actively the composition of cancer, color may not consider that immunospecifically binds to a 121PIF1 related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody the variable domains of the heavy and light chains of a monoclonal color antibody), a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes as a fingle comprisive, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121PIF1, inhibiting growth of cancer cells that expresses comprising administering to the cells the composition), treating a patient who bears cancer cells that expresses 121PIF1 (comprising administering to the cells the composition), treating a patient who has or who is suspected of cancer cells that expresses comprise a polynucleotide in a biological sample from a patient who has or who is suspected of having cancer, monitoring the composition may comprise a polynucleotide that comprises a 121PIF1 composition may comprise a polynucleotide that comprises a 121PIF1 composition may comprise a polynucleotide that encodes at least one composition may comprises a polynucleotide that encodes at least one composition is useful for detecting, the peptides of the encode the entire amino acid sequence of 121PIF1 (ADM83793. The composition is useful for detecting, treating or comprises a polynucleotide that encodes at least one comprises a polynucleotide that encodes at least one composition is useful for detecting, treating or its splice variants. The composition is useful for detecting, treating or its splice variants. The composition is useful for detecting, treating or composition to treat or prevent cancer, badder cancer, badder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, badder cancer, kidney cancer, badder cancer as a composition to a supposition can also be 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                               03-JUN-2004
                                                                                          ADM83835;
                                                                                                                                     ADM83835 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
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lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                          RTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCERIGTSNYYWAFPSKALHARKHKLEVLES-QLSEGSQKHASLQKSIEKAKIGRCETEE
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                                               (first entry)
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Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4g; HLA; human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer; colon cancer; human ancreatic cancer; bancreatic cancer; brast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                Human cancer gene 121P1F1 variant
                                                                                                                                                                                                                                                                                          lung cancer; purcer; er; stomach cancer;
                                                                                                                                                                                                                                                                                                                 protein
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Homo sapiens

US2003223997-A1.

28-FEB-2002; 2002US-00087190

08-FEB-2001; 2001US-00779250

(RAIT/) (HUBE/) (CHAL/) HUBERT R S.
RAITANO A B. CHALLITA-EID P M.

(AFAR/) (FARI/) AFAR DEH. GEW. JAKOBOVITS A. FARIS

Challita-Eid PM, Hubert RS, Raitano AB, Faris Z, Afar ဝူ

Ξ

WPI; 2004-060522/06

New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast ç

Example 5; SEQ ID NO 45; 211pp; English

Composition comprising the modulated by 121PIF1 where status of the cell composition comprising the movel composition in a human unit does form, a crecombinant protein comprising an antigen-binding region of a monoclonal composition that produces an antibody, a single chain monoclonal antibody, a non-human transgenic animal that produces an antibody, a chain monoclonal antibody contain the variable domains of the heavy and light chain so f a monoclonal antibody contain monoclonal antibody, a polynucleotide that encodes an analogue chain monoclonal antibody, a polynucleotide that encodes an analogue chain monoclonal antibody, a polynucleotide that encodes an analogue chain monoclonal antibody, a polynucleotide that encodes an analogue chair that expresses 121PIF1, inhibiting growth of cancer cells that expresses 121PIF1, inhibiting crowth of cancer cells that expresses (121PIF1 (comprising administering to the cells that expresses (121PIF1 (comprising administering to the cells that expresses (121PIF1) (comprise (121PIF1) (composition) (comprise (121PIF1) (composition) (composition) (comprise (121PIF1) (composition) (comprise (121PIF1) (composition) (compos The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer exp expressed

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RESULT 12
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        The invention relates to a composition comprising a substance that modulates the status of 121PIF1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121PIF1 where status of the cell that expresses 121PIF1 is modulated. Also included are a pharmaceutical
                                                            Example 2; SEQ ID NO 24; 211pp;
                                                                                         treating or preventing cancer
                                                                                                     New composition comprising 121P1F1 or a molecule that
                                                                                                                                    WPI; 2004-060522/06.
                                                                                                                                                        Challita-Eid PM,
Jakobovits A;
                                                                                                                                                                                                                      (CHAL/)
(HUBE/)
(RAIT/)
(FARI/)
                                                                                                                                                                                                                                                                         08-FEB-2001;
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(GEWW/)
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                                                                                                                                                                                                                                                                                                                                                                            cancer; stomach cancer; gene therapy; vaccine.
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HUBERT R S.
RAITANO A B.
                                                                                                                                                                                       JAKOBOVITS
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GEW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCERIGTSNYYWAFPSKALHARKHKLEVLESQELSEGSQKHASLQKSIEKAKIGRCETEE
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                                                                                                                                                                  Hubert
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                                                                                                                                                                  RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                         a substance that modulates the status of is modulated by 121P1F1, useful for detecting, cer e.g. prostate, bladder, colon, breast or
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                                                                                                                                                                  Raitano AB,
                                                             English.
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                    cell
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Homo

Bapiens

eukaemia.

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC chain monoclonal antibody, a polynucleotide that encodes an analogue that expresses 121P1F1, inhibiting growth of cancer cells that expresses (21P1F1), inhibiting growth of cancer cells that expresses (21P1F1) (comprising administering to the cells the composition), treating (21P1F1) (comprising administering to the cells the composition), treating (21P1F1) (composition) and (21P1F1), inducing an immune response directed to 12P1F1, inducing an immune composition of composition and (21P1F1) gene products in a biological sample from a composition of cancer in an individual and an assay for detecting the composition may comprise a polynucleotide that comprises a 12P1F1. The composition may comprise a polynucleotide that comprises a 12P1F1. CC related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 12P1F1 (ADM83793). The composition is useful to be peptides a polynucleotide that encodes at least one composition is useful for detecting, treating or compressed concer, preferably prostate cancer, breast cancer, kidney cancer, colon cancer, lung cancer, prostate cancer, breast cancer, kidney cancer, colon cancer, lung cancer, prostate cancer, breast cancer, kidney cancer, colon cancer.
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Matches
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                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as vaccine to treat or prevent cancer that expresses or overexpresses 121PIFI. The gene for 121PIFI is located on chromosome 4q. The present sequence is a 121PIFI protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 1211F11-related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody), a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes an analogue
                                                                                                                                                                                                      Human polypeptide
                                                                                                                                                                                                                                                  22-OCT-2001
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Pred. No. 3.6e-85;
0; Mismatches 0;
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WO200153312-A1

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RESULT 14
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Matches 190;
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                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, contained and peripheral nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity second as: Immune system suppression, activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the peripheral specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999;
21-JAN-2000;
25-APR-2000;
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Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                  Sequence 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 3188; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating as central nervous system injuries.
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19-OCT-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                            Local Similarity
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Wang Z,
Goodrich
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Wehrman T,
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nrman T, Xu C,
Drmanac RT;
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ADD84547

standard;

protein; 190

GIPEDFDYID

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CC The present invention describes a composition (I) comprising a substance chat modulates the status of 121PIF1 (gene and encoded protein), or a cc molecule that is modulated by 121PIF1 (where the status of a cell that c expresses 121PIF1 is modulated. The human 121PIF1 gene maps to chromosome CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in cytosticating or treating patients with cancer that expresses 121PIF1 geness, cc prognosticating or treating patients with cancer that expresses 121PIF1 geness, can be used to elloit a humoral or cellular immune response. CC fragment can be used to elloit a humoral or cellular immune response. CC 121PIF1 antibodies can be used in active or passive immunisation. 121PIF1 genes, as coding sequences for the amplification or cettorion of 121PIF1 genes, as coding sequences for directing the expression of 121PIF1 polypeptides, or as tools for modulating or inhibiting the expression of 121PIF1 genes. The present sequence is used in the exemplification of the present invention.
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Best Local Similarity
Matches 190; Conserv
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                                                                                                                                                                                                                                                                                                         Sequence
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DB; ADD84546.
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                                                                                                         SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE 120
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100.0%; Pred. No. 7.3e-82;
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RESULT 15
ADM83857
chain monoclonal antibody, a polynucleotide that encodes a single peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121P1F1, inhibiting growth of cancer cells that expresses 121P1F1, inhibiting growth of cancer cells that expresses 121P1F1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that expresses 121P1F1, generating a mammalian immune response directed to 121P1F1, inducing an immune response of manifering 121P1F1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the presence of cancer in an individual and an assay for detecting the presence of a 121P1F1-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that comprises a 121P1F1 related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 121P1F1 (ADM83793. The substance also comprises a polynucleotide that encodes at least one polynucleotide given in 16 Tables (given in the specification), the peptides
                                                                                                                                                                                                                                                                                                                                                              recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a constituent of the produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising that variable domains of the heavy and light chains of a monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulates the status of 121P1Fi (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition comprising a substance that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; SEQ ID NO 67; 211pp; English
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HUBERT R S.
RAITANO A B.
FARIS M.
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                                                                                                                    100%
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                                                                                                                                                                                                                  283416
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

. 29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	_U	4.	ω	N		NO.	Regult	
109	109.5	109.5	109.5	109.5	109.5	109.5	110	110.5	110.5	110.5	111	111	112	112	112	112	113	114	114	115.5	116.5	117	121.5	130.5	135.5	168.5	197	349	Score	•	
10.4	10.5	10.5	0		0	10.5	0	0	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.7	10.8	10.9	10.9	11.0	11.1	11.2	•	12.5	12.9	16.1	18.8	33.3		Query	æ
284	1390	1298	400	284	168	168	284	879	629	308	1937	559	1938	559	285	284	199	764	284	880	2442	768	1356	1053	1281	174	. 128	210	Length		
N	N	N	N	N	N	N	N	N	N	N	ນ	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	ผ	80	}	
JC2551	S51364	T24480	E70318	JC6198	B72046	G86578	151731	C71083	T44607	T08796	I38055	A45620	A59293	S49143	A24199	JC6199	A32183	T05409	S24972	F75103	T08621	T02572	S32763	A41642	JC5368	861134	T08972	T37610	10	}	
tropomyosin aipha	sperm tail-specifi	hypothetical prote	hypothetical prote	alpha-tropomyosin	conserved hypothet	CT670 hypothetical	alpha-tropomyosin	conserved hypothet	hypothetical prote	tropomyosin - huma	myosin heavy chain	cytovillin homolog	skeletal myosin he	EG10 protein - tap	tropomyosin NM, sk	alpha-tropomyosin	tropomyosin TPM1 -	hypothetical prote	tropomyosin alpha,	conserved hypothet	centrosome associa	hypothetical prote	kinectin 1 - human	dynactin - chicken		ical	hypothetical prote		Description		

hypothetical protein F19B15.200 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: T08972 R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, May 1999 A;Accession: T08972

A;Molecule type: DNA

RESULT 2 T08972

4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30
106.5	107	107	107	107	107	107	107	107	107.5	107.5	107.5	108	109	109
10.1	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.3	10.3	10.3	10.3	10.4	10.4
1558	955	284	284	284	284	284	281	280	1169	1137	1085	670	676	284
N	N	N	N	N	N	۲	N	N	N	N	N	N	N	N
B71603	S24348	A60597	A25825	B27407	A39816	TMRBA	A34787	A22165	A64505	T19414	F96712	F84899	S00084	819691
RESA-H3 antigen PF	myosin heavy chain	tropomyosin 2, fib	tropomyosin alpha	tropomyosin alpha	tropomyosin 2, fib	tropomyosin alpha	tropomyosin 1 alph	tropomyosin alpha	P115 homolog - Met	hypothetical prote	hypothetical prote	hypothetical prote	myosin heavy chain	tropomyosin alpha,

ALIGNMENTS

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T37610
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R;Hunt, S.; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the SMBL Data Library, September 1995
A;Reference number: Z21730
A;Accession: T37610
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A; Introns: 22/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-210 <HUN>
A;Cross-references: UNIPROT:Q09739; UNIPARC:UPI0000139F78; EMBL:Z54096; PIDN:CAA90804.1;
A;Experimental source: strain 972h-; cosmid c13A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.3%; Score 349; DB 2; Length 210; Best Local Similarity 41.6%; Pred. No. 3.3e-16; Matches 84; Conservative 36; Mismatches 76; Indels
                                                    181
                                                                                                      123
     183
                                                                                                                                                     122 RLAKELSSLRD-QREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
                                                                                                                                                                                                       63
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                                                                                                                                                                                                                                                                                                      4 KGLSLAEKRRRLEAIFHDSKDFFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK 62
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                                                                                                                                                                                                                                 IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI--EKAKIGRCETE-ERT 121
                                                    KRKFGFEENKIDRTFGIPEDFD 202
                                                                                                 OYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC
                                                                                                                                                                                                       IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 122
                                                                                                                                                                                                                                                                                                                                          KGLSABEKRTRMMEIFSETKDVFQLKDLEKIAFKEKGITAMSVKEVLQSLVDDGMVDCER 64
-RDMGADTNOIREYCSIPEDLD 203
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RESULT 4
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S61134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V. submitted to the EMBL Data Library, September 1995
A;Description: The sequence analysis of a 7.9 kb DNA fragment from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YGL183c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein G1604

C;Species: Saccharomyces cerevisiae

C;Date: 23-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: S61134; S64200

C;Accession: S61134; S64200
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A;Residues: 1-128 <BEV>
A;Cross-references: UNIPROT:Q9SZE5; UNIPARC:UPI00000AAA02; EMBL:AL078470; GSPDB:GN00062;
A;Experimental source: cultivar Columbia; BAC clone F19B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000013B11A; EMBL:Z72705; NID:g1322796; PIDN:CAA96895.1;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-174 <BRU>
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A; Accession: S64200
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A; Residues: 1-174 <BER>
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A;Accession: S61134
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;Introns: 13/3;
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Best Local (
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Best Local Similarity
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                                                                                      120
                                                                                                                              157
                                                                                                                                                                                                 104 QKSIEKA-KIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
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                                                                                                                                                                                                                                                         1 MIVKDLVOOMIDEDGVISVEKCGNINIYWCFKNQTLQKLYDSSELIKKKIQEVKCDIATY
                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                         KQELDKTLATGRRKKFTVGQKSYNRBALLEKRKKIQDEIKK-KSNSLQKIESIRWDAAKI
                                                                                                                              QANK-----VAKEAANRWIDNIFAIKSWAKKFGFEENKIDRIFGIPEDF 201
                                                                                      QENKQQIRLKKVHLEKTTDNIEILIDYLYKKFFLKPEQIRKEFGIPEEF 168
                                                                                                                                                                                                                                                                                                   MSVKEVLQSLVD-DGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASL 103
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                16.1%; Score 168.5; DB
27.2%; Pred. No. 0.0002;
tive 42; Mismatches 6
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Pred. No. 1.9e-06;
23; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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dynactin 1 - mouse
N;Alternate names;
C;Species: Mus muscu
C;Date: 28-May-1997
C;Accession: JC5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Pate: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C;Accession: A41642
C;Accession: A41642; MUID:92098576; PMID:1836789
A;Reference number: A41642; MUID:92098576; PMID:1836789
A;Accession: A41642
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R;Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.
Blochem. Biophys. Res. Commun. 231, 344-347, 1997
A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate A;Reference number: JC5368; MUID:97223454; PMID:9070275
A;Accession: JC5368; MUID:97223454; PMID:9070275
                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1053 <GIL>
A;Cross-references: UNIPROT:p35458; UNIPARC:UPI000017C003; GB:X62773; NID:g63920; PID:g6
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
A41642
dynactin - chicken
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A;Residues; 1-1281 <JAN>
A;Cross-references: UNIPROT:O08788; UNIPARC:UPI0000027AAD; GB:U60312; NID:g2104494; PIDN
A;Experimental source: brain
C;Comment: This protein is a member of the oligomeric dynactin complex that is required
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A;Map position: 6
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                                                                                                                                                                                      101 AKKEAKDALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVDSLKEKVEYLTMD 160
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                                                                                                                                                                                                                                     2 SKKKGLSABEKRTRMMSIFSETKDVFQLKDLEKIAPKEKGITAM----SVKEVLQSLVDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIGRCET--EERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVBEIRQANKVAKEAANR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CERI-----GTSNYYWAFPSKALHAR-KHKLEVLESQLSEGSQKHASLQKSIEKA 110
                                                                                           LEILKHEIEEKGSDGAASSYQVKQLEEQNARLKEALVRMRDLSASEKQEHVKLQKQMEKK 220
                                                                                                                                       GMV---DCERIGTSNYYWAFPSKALHARKHKLE---VLESQLSEG-SQKHASLQKSIEKA 110
                                            KIGRCETEERTRLAKELSSLRDQREQLKASVEK-YKDCD------PQVVEEIRQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNQELEVVRQQRERLQEELSQAESTIDELKEQVDAALGAE-EMVEMLTDRNLNLEEKVRE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                          12.5%;
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-TELESLROOREKLOEEVKOAEKTVDELKEOVDAALGAEEMVETLTE
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Pred. No. 0.25;
3; Mismatches 106;
                                                                                                                                                                                                                                                                                                            Score 130.5; D
Pred. No. 0.44;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                     DB 2;
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ANKVAKEAANRWIDNIFAIKSWAKRKFGFEENKIDRIFGIPEDFD

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1356 <KRUy
A;Cross-references: UNIPROT:Q86UP2; UNIPARC:UPI00000702A8; EMBL:Z22551
A;Cross-references: UNIPROT:Q86UP2; UNIPARC:UPI00000702A8; EMBL:Z22551
A;Cross-references: UNIPROT:Q86UP2; UNIPARC:UPI00000702A8; EMBL:Z22551
A;Cross-references: UNIPROT:Q86UP2; UNIPARC:UPI00000702A8; EMBL:Z22551
A;Cross-references: Control of Co
                                                                                                                                                                                                                                                                                                                                                                                        NyAlternate names: hypothetical protein T16B24.6
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02572; F84815
C;Accession: Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: S32763; I37947
R;Kruppa, G,; Fuetterer, A.; Lemke, H.; Kroenke, M.
submitted to the EMBL Data Library, April 1993
A;Description: Cloning and characterization of TAF, a novel tran
A;Reference number: S32763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
A;Residues: 1-768 <ROU>
A;Cross-references: UNIFROT:080951; UNIFARC:UPI00000A1172; EMBL:ACC004697; NID:g3402671; A;Experimentel source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1356 <RES>
                                                                                                                                                                                                                  A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                         A; Reference number: Z14679
A; Accession: T02572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein At2g39300 [imported] - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinectin 1 -
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKKNNDLREKNWEAMEALASTEKMLQDKVNKTSKERQQQVEAVELEAKEVLKKLFPKVSV
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Pred. No. 2.2;
31; Mismatches
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                          C.Y.;
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A;ReBidueB: 1-768 <STO>
A;Cross-references: UNIPARC:UPI00000A1172; GB:AE002093; NID:g3402677; PIDN:AAC28980.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: F84815
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A;Tille: Autoantibodies to a group of centrosomal proteins A;Reference number: Z16462; MUID:98165428; PMID:9506584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 11-Jun-1999
C; Accession: T08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      centrosome associated protein CEP250 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-2442 < MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T08621
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A;Map position: 2
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                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Experimental source: cell line
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1821
                                                                                                                                           1714 KGPSKAQRGSLEHMKLILRDKEKEVECQQEHIHELQELKDQLEQQLQGLHRKVGET----
                                                                                                                                                                                                                  1662 LOKERIOVLEDORTROTKILEE------DLEOIKLSLRERGRELTTOROLMQERAEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 AFEVLSLIRSOMDERASTREDIRRVKNOWDLLLKRIEKEKTELOVOLETELDRRSSEWTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80/2;
                                                                                                                                                                                                                                                                                          46;
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                                                                                                                                                                                                                                       1 MSKKKGLSABEKRTRMMEIFSETKDVFQLKDLE--KIAPKEKGITAMSVKEVLQSLVDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSKKKGLSAE-----EKRTRMMEIFSETK-----DVFQL-KDLEKIAPKEKGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KVESFKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEV-LESQLSEGSQKHAS
                                SLRDQREOLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELSATAEEMREENLFLMQNLSKLQESYT-
ALQQEQQQAQGQEERVKEKADALQGALEQAHMTLKERHGELQDH----KEQARR 1870
                                                                    ---SILLSQREQEIVVLQQQLQEAREQGELKEQSLQSQLDBAQRALAQRDQ-----ELE
                                                                                                         AFPSKALHARKHKLEVLESQLSE----GSQKHASLQKSIEKAKIGRCETEERTRLAKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KE----AANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDFDYI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCKEDDVSSELEKRYKEAEKRVKLLSEEMEEKKFLSDCDFDISSLVGDIRQMEEERVGL-
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                          Score 116.5;
Pred. No. 9;
47; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            from
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Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.; Fritzler, M.J.; Rattner, J.B
                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                            64;
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                                                                                                                                                                                                                                                                                                                                 2442;
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                                                                                                                                                                                 --RIGTSNYYW
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                                  182
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                                                                                                           128
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Вb
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S24972
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                                                                                                                                                                                                                                                                                                                              R;Whitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Xie, X.; Hatch, submitted to the EMBL Data Library, April 1992
A;Description: Structure of tropomyosin at 9 Angstroms resolution.
A;Reference number: S24972
A;Accession: S24972
                                                                                                                                                                                                                                                                                                                                                                                                                           tropomyosin alpha, cardiac - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S24972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: PAB0812
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-880 <KAW>
A;Cross-references: UNIPROT:Q9UZC8; UNIPARC:UPI0000034523; GB:AJ248286; GB:AL096836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: Pyrococcus abyssi genome sequence: insights into A;Reference number: A75001 A;Accession: F75103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: F75103
R;anonymous, Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein PABO812 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-284 < WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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Best Local S
Matches 58
                                                                                                                                                                                                            ;Cross-references: UNIPROT:P42639; UNIPARC:UPI000013724F; EMBL:X66274; NID:g1926; PIDN;Superfamily: tropomyosin;Keywords: cardiac muscle; heart
                                                                                                                                       Matches
                                                                                                                                                                           Query Match
                                                                                                                                                           Local
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                     58
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                                                         73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                               1 MSKKKGLSAE---EKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDD
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNERMKAIEELRKAKGKCPVCGRELTEEHK--KELMERYTLEIKKIEEELKRTTE-EERK 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEELEDAKQVQKQIERLKARLKGLSPGEVIEKLESLEKERTEISEAIKEITTRIGQMEQE 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKKGLEEKIVQIERSIEEKKAKISELEEIVKDIPKLQEKEKEYRKLKGFR------
LAEKKATDAEADVASLNRRIQLFEEELDRAQ----ERLA-----TALQKLEEAEKAADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKSIEKAK-----
                                                                                                                                                       10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 115.5; 1
24.1%; Pred. No. 3.5;
Live 38; Mismatches
                                                                                                                                     37;
                                                                                                                                     Score 114; DB Pred. No. 1.3; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -IGRCET--EERTRLAKELSSL-----RD 132
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                                                                                                                                   61;
                                                                                                                                                                           Length
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                                                                                                                                       74;
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                       100
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RESULT 12
A32183
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R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, submitted to the Protein Sequence Database, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F10M6.170 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
T05409
                                                                                                                                                                                                                                                                                                         Cell 57, 233-242, 1989
A;Title: Disruption of the single tropomyosin gene in yeast results in the disappearance A;Reference number: A32183; MUID:89195234; PMID:2649250
                                                                                                                                                                                                                                                                                                                                                                                tropomyosin TPM1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2332; protein YNL079c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Sep-1989 #sequence revision 08-Sep-1989 #text_change
C;Accession: A32183; S53899; S63011; S63018; S63928
R;Liu, H.; Bretscher, A.
                                                                                                                                                   A;Cross-references: UNIPROT:P17536; UNIPARC:UPI0000137254; R;Poehlmann, R.; Philippsen, P. submitted to the EMBL Data Library, April 1995
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A;Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1; R;Poehlmann, R.; Philippsen, P.
                                                  A; Molecule type: DNA
A; Residues: 1-199 < POE>
                                                                                                      A; Reference number: S53896
A; Accession: S53899
                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-199 <LIU>
                                                                                                                                                                                                                                                                                 A; Accession: A32183
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A; Note: F10M6.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:O49371; UNIPARC:UPI00000A7B02;
A;Experimental source: cultivar Columbia; BAC clone F10M6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-764 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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A;Accession: T05409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 ERTRLAKELSSLRDOREOLKAEVEKYKOCDPOVVEEIRQANKVAKEAANRWTDNIFAIKS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 LHDAERKLISD-----KNKLNRAKEELEKREKTISEASIKHESLQEELKRANV---ELA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 MVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEK-----GITAMSVKEVLQSLV--DDG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKYEEEIKVLSDKLKEAETR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVARKLVIIESDLERABERAELSEGKC-----AELEEELKTVTNNLKSLEAQAEKYSQKE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAESANVLFDKLFARTHRLERQTNQHSVYPDDDDDLPYSNLGVLESDLEAALVALLKREED 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ASIQKSIEKAKI--GRCETEERTRIAKELSSLRDQREQLKAEVEKYKDCD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERGM--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 114; DB 22.8%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KVIESRAQKDEEKMEIQEIQLKEA--KHIAEDADRKYE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AEFAERSVTKLEKSID
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                                                                                                                                                                                                          EMBL: M25501; NID: g173037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AL021811
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A;Gene: ATmS-1
C;Superfamily:
C;Kgywords: act
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A;Residues: 1-199 <POW>
A;Cross-references: UNIPARC;UPI0000137254; EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1;
A;Experimental source: strain S288C
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                             RiLuque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F. Gene 185, 175-180, 1997
A;Title: Differential expression of a novel isoform of alpha-tropomyosin in A;Reference number: JC66.98; MUID:97208870; PMID:9055812
A;Contents: skeltal muscle
                                                                                                                                                                                                                                                                                                            alpha-tropomyosin S-1 - axolotl C;Species: Ambystoma mexicanum (axolotl) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004 C;Accession: JC6199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: 14L
C, Superfamily: slime mold ribozyme I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-199 <POF>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
                                                                                                                                 A;Accession: JC6199
A;Molecule type: mRNA
A;Residues: 1-284 <LUQ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SGD:TPM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 12, 391-402, 1996
A;Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals
A;Reference number: 863925; MUID:96267764; PMID:8701611
A;Accession: 863928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain S R; Poehlmann, R.; Philippsen, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S63018
A; Accession: S63018
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A;Accession: S63011
                                                                     C; Genetics:
                                                                                       A; Cross-references: UNIPROT: P87349; UNIPARC: UPI00000FB5F3; GB: U33450; C; Comment: This protein is a actin-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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A;Cross-references: UNIPARC:UPI0000137254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Genetics:
;Superfamily: tropomyosin
;Keywords: actin binding
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 HASLOKSIEKAKIGRCETEERTR-----LAKELSSLRDOREOLKAEVB----KYKDC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQVVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQQLEEDLEBSDTKLKETTEKLRESDLKADQLERRVAALEEQREEWERKNEELTVKYEDA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCERIGTSNYYWAFPSKALHARKHKL----EVLESQLSEG-------SQK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKELDE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSKQTEQDNVEKENQIKSLTVKNHQLEEEIEKLEAELAESKQLSEDSHHLQSNNDNFSKK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEASSWORKYEELKEKOKDLEO-ENVE----KENOIKSLTVKN--OOLEDEIEKLEAGLS
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                                                                                                              NID:g1871357;
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                                                                                                                 PIDN
                         RESULT 15
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A;Cross-references: UNIDARC:UPI000013D90D R;Reinach, F.C.; MacLeod, A.R. Nature 322, 648-650, 1986
A;Title: Tissue-specific expression of the A;Reference number: A24199; MUID:86311274; A;Accession: A24199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Clayton, L.; Reinach, F.C.; Chumbley, G.M.; MacLeod, A.R. J. Mol. Biol. 201, 507-515, 1988
A;Title: Organization of the hTM(nm) gene. Implications for A;Reference number: S02554; MUID:88332987; PMID:3418707
A;Accession: S06210
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI000013D90D; GB:X04201; NID:g37429; PIDN:CAA27798.1; A;Note: an intronless pseudogene resembling this mRNA is also known C;Superfamily: tropomyosin C;Keywords: alternative splicing; coiled coil; muscle; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change
C;Accession: S06210; A24199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-285 < REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-285 < CLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tropomyosin NM, skeletal muscle - human
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nes 52; Conserv
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231
                                                                                                                              108
                                                                                                                                                                     134 R----ALKDEEKMELQEI-------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AKEAANRWTDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 R----ALKDEEKMELQEI-------QLQEAKHIAEEADRKYEEVARKLVIIEGDL
                                                                                                                                                                                                                48 KEVLOSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK----HASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                              74 LAEKKAADAEAEVASINRRIQIVEEELDRAQERLATALQKLEEAEKAADESERGMKVIEN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                          1 MSKKKGLSAEEK---RTRMMEIFSETKDVFQ-----LKDLEKIAPK-EKGITAMSV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKKKGLSAEE---KRTRMMEIFSETKDVFQ-----LKDLEKIAPK-BKGITAMSV 47
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                                         KVAKEAANRWIDNIFAIKSWAKRKFGFEENKIDRIFGIPED 200
                                                                                                                         EKAKIGRCETEERTRIA-----KELSSLRDQREQLKAEVEKYKDCDPQVVEBIRQAN
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41; Mismatches
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(Echinococcus

granulosus)

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C;Species: Echinococcus granulosus
C;Ste: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 15-Mar-2004
C;Accession: S49143
R;Frosch, P.M.; Hartmann, M.; Sygulla, L.; Margutti, P.; Frosch, M.
submitted to the RMBL Data Library, January 1994
A;Description: Identification of a cDNA clone from the larval stage of Echinococcus gran A;Reference number: S49143
A;Reference number: S49143
A;Retextion: S49143
A;Retextion: S49143
A;Retextion: From S49143
A;Retextion: Freiminary
A;Molecule type: mRVA
A;Residues: 1-559 <FRO>
A;Residue
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Search completed: February
Job time : 45 secs
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Q5XYY9_XENLA
Q4S906_TETMQ
Q6C61_BRARE
Q86EZ8_SCHDA
Q6H432_ORYSA
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Q5CR3_CRYNE
Q7SCH5_ARDDA
Q5CR3_CRYNE
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Q7SCH5_ARATH
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Q9BWT6; Q9BWT6; Q1-JUN-2001 (TrEMBLrel. 17, Q1-JUN-2001 (TrEMBLrel. 30, QAJ. Name=GAJ; Homo sapiens (Human). Eukaryota; Metazoa; Chordat Mammalia; Eutheria; Euarche Homo. NCBI TaxID=9606; [1] — TAXID=9606; [2] — NUCLEOTIDE SEQUENCE. TISSUE=Lymph; DAVABURATE S., Morley K.C., Morl	1153.5 1153.5 1153.5 1154.5 1154.5 1154.5 1154.5 1154.5 1154.5 1154.5 1154.5 1154.5
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PRELIMINARY; TrEMBLrel. 17 TrEMBLrel. 27 TrEMBLrel. 30 G; GUENCB. GUENCB. GUENCE. 257; PubMed=1 L. Feingold Colling F.S Zeeberg B., Zeeberg B., Zeeberg B., Jordan H., M Marusina K. Zoaren R.J., Marusina K. Marusina K. Worley K.C., Muzny D.M., Lone M. B. J., Usdin T.B. J., Warland J. J., All J. J., Mndl. J. J., Mndl. J.	101 2 101 2 1395 2 1281 1 1289 2 890 2 1129 2 1139 2 11278 1 1278 1 1278 1
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vertebrata; Euteleostomi; imates; Catarrhini; Hominidae; imate	Q5csy4 cryptospori Q6e679 antonospora Q7t2f8 brachydanio Q4ssb9 tetraodon n 008788 mus musculu Q59f36 homo sapien Q6awb1 homo sapien Q6awb3 homo sapien Q6iq37 homo sapien Q6nzm3 mus musculu Q1203 homo sapien Q6mzz3 homo sapien Q5rds4 pongo pygma P28023 rattus norv

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Best Local Similarity
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01-OCT-2002
01-OCT-2002
                EMBL, BC027741; AAH27741.1; -; mRNA.
Ensembl; ENSMUSG00000033752; Mus musculus
MGI; MGI:1924165; 2610034E18Rik.
InterPro; IPR005647; Mnd1.
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna; Muroldea; Muridae; Murinae; Mus.
  SEQUENCE
                                                   Submitted (APR-2002) to the EMBL/GenBank/DDBJ
                                                          TISSUE=Mammary tumor metastatized Director MGC Project;
                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse) .
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                                                                                                                                                                                                                                                                                                      SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                      Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
  $
           Mnd1;
                                                                                                     Sci.
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  23849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                      U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                 22,
                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1047; DB 2;
Pred. No. 8e-57;
  122C3FA9E4325120 CRC64;
                                                                   to lung. Tumor arose spontaneously;
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RESULT

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                                                                                                                                                                                                                                                                 RX KADDINE=21085660; Phibmed=11217851; DOT=10.1038/35055500; RRA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA KAWAI J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Shiburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H.A., Shiburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H.A., Nikaido I., Pesole G., Quackenbush J., Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Schriml I.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Flutno M., Aono H., Baldarealli R., Barsh G., Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Blake J., Bolt C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N. H., Ba Baki H., Sato K., Scheenbach C., Seya T., Shbata Y., Storch K.-F., Sasaki H., Sato K., Scheenbach C., Seya T., Shbata Y., Storch K.-F., Sanaka H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wansaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local 9
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610034E18 product:GAJ homolog.
Name=2610034E18Rik;
                               STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DOA1 MOUSE PRELIMINARY;
                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                     ional annotation of 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cy full-length cDNA cloning.";
303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.1%;
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                                                                                                                                                                                                                 full-length
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Pred. No.
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                                                                                                                                                                                                                        collection.";
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                                  Team;
         annotation
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RESULT 4
OSFV93 XENTR
ID QSFV93_XENTR PRELIMINARY;
AC QSFV93;
DT 10-MAY-2005 (TrEMBLrel. 30,
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RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojina Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Kawai J., Kojina Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Kawai Y., Okido T., Owa C., Salto R., Sakai C., Sakai K.,

A Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C., Sakai K.,

RA Okazaki Y., Okido T., Toya C., Salto H., Saito R., Sakai C.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Rejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

RA Muramatsu M., Hayashizaki Y.;

REMBL, AKO11664; BAB27765.1; -; mRNA.

EMBL; AKO11664; BAB27765.1; -; mRNA.

REMBL; BRSMUSG00000033752; Mus musculus.

PR MGI: 1924165; 2610034E18Rik.

PR MGI: 1924165; 2610034E18Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/60; TISSUE-Whole body;

MEDLINE-20530913, PubMed-11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                  183;
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420:563-573(2002).
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||||||||||||||::|| |||||
DCERIGTSNYYWAFPSKALHARKRKLEALNSQLSEGSQKHADLQKSIEKARVGRQETEER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             90.5%; Score 948; DB
89.3%; Pred. No. 9.6e
tive 10; Mismatches
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.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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RESULT
Q5XGY9
ID Q7
AC Q7
D7 22
D7 22
D7 22
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D7 21
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RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsish F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schuern J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT proc. Natl Asad Schl U.S. a 40.16404-16401/20021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
LOC495113 protein.
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SEQUENCE 205 AA; 24130 MW;
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Submitted (FEB-2005) to the
EMBL; BC090139; AAH90139.1;
InterPro; IRR005647; Mnd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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10-MAY-2005 (TrEMBLrel.
                                                                                        Q5XGY9;
                                                                                                         Q5XGY9_XENLA
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Name=MGC97859;
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                                                                                                                                                                                                                                                                      SKLABELASRRHRKEELCABLEKYKECDPDVIBEIRQSNKVAKDAVNRWTDNIFAVKSWA
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                                                                                                                                                                                                                               KRKFGFEENKIDRTFGIPEDFDYID
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                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%; Score 848; DB 2;
77.1%; Pred. No. 1.3e-44;
tive 29; Mismatches 18
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-; mRNA.
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                                 annotation update)
                                                    sequence update)
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LOC495113 protein Name=LOC495113;

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Jordan J., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rahesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
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Best Local
   ILT 6
106 TETNG
Q4SS06 TETNG
Q4SS06;
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Gerhard D.S.; submitted (CCT-2004) to the EMBL; BC084288; AAH84288 1; InterPro; IPR005647; Mnd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
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                                                                                                                                                                                                                                                                                               SKLVEELASLRHRKEELCADLEKYKECDPDVVEEIRQSNKVAKDAVNRWTDNIFAVKSWA
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l. Acad. Sci. U.S.
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                                    PRELIMINARY;
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Pred. No. 1.3e-
27; Mismatches
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                                    PRT;
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RESULT
Q6DC61
ID Q6
AC Q6
DT 255
DT 255
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CGN OFF

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

Created)
Last sequence update)
Last annotation update)

28, 28, 28,

QEDC61_BRARE QEDC61;

PRELIMINARY;

PRT;

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BRARE

25-OCT-2004 (TrEMBLre 25-OCT-2004 (TrEMBLre 25-OCT-2004 (TrEMBLre 25-OCT-101017) 25-OCT-2004 (TrEMBLre 25-OCT-

(Zebrafish) Chordata;

Craniata; (Danio

Vertebrata;

Euteleostomi;

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13-SEP-2005 (T
13-SEP-2005 (T
Chromosome 18
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Bukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
ORFNames=GSTENG00013672001;
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                       Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry which
                                                                                                                                                                                                                                                                                                                                          the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                              preliminary data
181
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                                                                                                                              KKFAFDENSINKAFGIPEDFDYLD
                                                       RLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAK
                                                                                    CERIGTSNYYWAFPSKVLHARKRKLEELQQQISQAKQRKASLVEAVEKAREGRQDTEERG
                                                                                                 CERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERT 121
             RKFGFEENKIDRTFGIPEDFDYID 205
                                          SLLKELKDLREERTRLLAQLEKYKDCDPEVVEEMRKSNVVAKAAVSRWTDNIFSIKSWTK
                                                                                                                                                                                                                     204 AA;
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(TrEMBLrel. 31, Last sequence update)
(TrEMBLrel. 31, Last annotation update)
18 SCAF14485, whole genome shotgun seque
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                     23844 MW;
                                                                                                                                                                                    74.8%; Score 783; DB 2; 72.1%; Pred. No. 1.3e-40;
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204
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DT 01-OCT-2
DE Clone ZE
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Richausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Richausner R.D., Collins F.S., Wagner L.H., Schaefer C.F., Bhat N.K.,

Ra Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Ra Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Ra Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ra Hopkins R.F., Jordan R., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ra Scapleton M., Gares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ra Roberts S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Ra Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Ra Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Ra Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Ra Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ra Hilaron B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ra Hilaron B., Krzywinski M.I., Skalska U., Smailus D.E.,

Ra Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Ra Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation Association of Mark Mark M. Marra M.A.;

Proc. Matl. Acad. Sci. U.S.A., 99:16899-16903 (2002).
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Best Local Similarity
                                                                                                                                                                                                                                    QBGEZB SCHJA PRELIMINARY; PRT; 1
QBGEZB;
QBGEZB;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequer
Q1-QT-2003 (TrEMBLrel. 25, Last annotation of the ZZD1259 mRNA sequence.
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Tischistosomatoidea; Schistosomatidae; Schistosomatoidea; Schistosomatidae; Schistosomatoidea; Schist
NUCLEOTIDE SEQUENCE.

MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;

MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;

Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,

Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu

Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03962; Mnd1;
SEQUENCE 220 AA;
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Cyprinidae; Danio.
NCBI_TaxID=7955;
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Director MGC Project;
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Pred. No. 4.8e-32;
0; Mismatches 29
                                                                                                                                                                                                                                                      Trematoda; Digenea; Schistosoma.
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                                                                                                                                                                                                                                                                       RC STRAIN-HM-1:IMSS;

RX PubMed=15729342; DOI=10.1038/nature03291;

RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

RA Amedeo P., Roncaglia P., Berziman M., Hirt R.P., Mann B.J., Nozaki T.,

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RA Fraser C.M., Hall N.,

"The genome of the protist parasite Entamoeba histolytica.";

RI Nature 433:865-868(2005).

CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                       Query Match
Best Local (
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Nat. Genet. 35:139-147(2003).
EMBL; AY223066; AAP06089.1; -; mRNA.
                                                                                                                                                                 preliminary data.
EMBL; AAFB01000572; EAL45733.1; -;
InterPro; IPR005647; Mnd1.
Pfam; PF03962; Mnd1; 1.
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Q50VW2_ENTHI PRELIMINARY;
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Pfam; PF03962; Mnd1; 1.
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196 AA; 2
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269 AA;
43.8%;
ilarity 42.9%;
Conservative 53
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                                                                                                                    31920 MW;
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47.4%; Pred. No. 6.4e-21;
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Last annotation update)
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Score 459; DB 2;
Pred. No. 1.4e-20;
3; Mismatches 64
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                                                                                                                    63AD3885CF0387B3 CRC64;
                                                                                                                                                                                                                                Genomic_DNA
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     64;
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                                                     Length 269;
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     Indels
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20 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BR105435; AAO63855.1; -; mRNA.

EMBL; BR005435; AAO63855.1; -; mRNA.

InterPro; IPR005647; Mnd1.

Prothetical protein.

SEQUENCE 230 AA; 26402 MW; 131BB5146D8C91ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Seki M., Iida K., Satou M., Sakurai T., Ak
Seki M., Iida K., Satou M., Sakurai T., Ak
Nakajima M., Enju A., Kamiya A., Narusaka
Nakajima M., Shinozaki K.;
Submitted (NOV-2002) to the EMBL/GenBank/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=At4g29170/F19B15_200; Synonyms=At4g29170;
Arabidopsis thaliana (Mouse-ear cress) Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
equresids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein At4g29170/F19B15_200 (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBGYD2_ARATH
QBGYD2;
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ARATH
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                                                                                                                                                         DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER
                                                                                                                                                                                      MSKKRGLSLEEKREKMLQIFYESQDFFLLKELEKMGPK-KGVISQSVKDVIQSLVDDDLV
                                                                                                                                                                                                    MSKKKGLSABEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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                  SNNFPQAKEQLEHLYTEAGITEDFDYIE
                                             KRKFGFEENKIDRTF--
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                                                                        TEALTQLKDIEKKHKDLKNEMVQFADNDPATLEAKRNAIEVAHQSANRWTDNIFTLRQWC
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                                                                                                                                                                                                                                                         42.0%;
                                -GIPEDFDYID
                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                          Score 440; DB
Pred. No. 1.7e
43; Mismatches
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ka M., Carninci P.,
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32 ORYSA
Q6H432 ORYSA E
                                Eichinger I., Pachebat J.A., Gloeckner G., Rajandream M.-A., Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q., Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P., Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C., Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Warten B., Van Driessche N., Cronin A., Goodhead I., Van Dries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SBP-2005 (TrEMBLrel. 31, Created)
13-SBP-2005 (TrEMBLrel. 31, Last sequence update)
13-SBP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=DDB0184048;
Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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Q54E86;
13-SEP-2005 (TremBirel. 3
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InterPro; IPR005647; Mnd1.
Pfam; PF03962; Mnd1; 1.
SEQUENCE 207 AA; 23900 |
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=AX4;
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genomic
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                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AV811553; AAX27442.1; -; mRNA.
InterPro; IPR000074; ApoAl A4 E.
InterPro; IPR010990; Cyt c b562.
InterPro; IPR011029; DEATH_like.
InterPro; IPR011029; DEATH_Like.
InterPro; IPR0019647; Mndl.
InterPro; IPR001993; Pt type.
InterPro; IPR0019976; PLAT_LH2.
InterPro; IPR0019976; PLAT_LH2.
InterPro; IPR0019976; Ming_hix_DNA_bd.
InterPro; IPR011991; Wing_hix_DNA_bd.
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Loulseged H., Mungall K., Oliver K., Pleter C., Quail M.A.,
Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schlaicher M., Weinstock G., Rosenthal A., Cox E.C.,
Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Schistosoma japonicum (Blood fluke).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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Q5BYT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 221 AA; 2
                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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SCHJA
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,; AAFI01000260; EAL61571.1; -; Genomic_DNA.
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CAUTION: The sequence shown here is derived from an
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                                                                                                              l Similarity
73; Conserv
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MSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQ 104
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161 AA; 1
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ilarity 45.6%;
Conservative 2
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                                                                                                                     28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 366; DB 2; 22
Pred. No. 5.7e-15;
                                                                                                                 Score 362; DB 2; I
Pred. No. 7.3e-15;
8; Mismatches 59;
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RA Holloyd G., Sanchez M., Schaekin J., Forsburg S.L., Ra Shpakovski G.V., Barrell B.G., Nurse P., Letter G., Forsburg S.L., Ra Shpakovski G.V., Barrell B.G., Nurse P., Letter G., Schizosaccharomyce
EMBL;
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01-NOV-1995 (Rel. 32, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
Meiotic coiled-coil protein 7.
Name=mcp7; ORFNames=SPAC13A11.03;
                                                                                               use
                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE, FUNCTION, AND INTERACTION WITH MEU13 PubMed=15210864; DOI=10.1093/nar/gkh654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes:
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Q09739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                               FUNCTION: Required for meiotic recombination. SUBUNIT: Interacts with meul3.
  AB189985; BAD42847.1; -; Genomic_
Z54096; CAA90804.1; -; Genomic_DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANRWIDNIFVIKSWLSNKFSLDEATFCRQFEIPENFDYI 160
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
EMBL; AL590449; CAD25881.1; -; Genomic_DNA.
InterPro; IPR005647; Mnd1.
Pfam; PF03962; Mnd1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein BCU10 1600.
OrderedLocusNames=ECU10 1600;
Encephalitozoon cuniculi.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
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Pfam; PF03962; Mndl; 1.
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COILED 77 148 Potential.

SEQUENCE 210 AA; 24224 MW; F4A546F070A37665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein. SEQUENCE 203 AA; 23743 MW; DFE33A65A1A28A42 CRC64;
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N9_ENCCU
Q8SUA9_ENCCU PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                  ch 32.5%; Score 340.5; DB 2; Length 2 l Similarity 35.1%; Pred. No. 1.9e-13; 71; Conservative 50; Mismatches 72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 122
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                                                               TSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKE 126
                                                                                                                               MKSDQKKSILLEIIRGSKSFFKLQELESLGSK-KGIVVNTIKEILQQLVDDGLVTAEKVG
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      TSNLYWSFASEGIQKKKLRCKELMEECERMSQDICRKREYIENEKMSKHYTEERNELENK 124
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Search completed: February 2, 2006, 12:51:01 Job time : 122 secs

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US-09-799-250B-72
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Sequence 2, Appli sequence 4, Appli sequence 4, Appli sequence 721, App sequence 721, App sequence 1321, App sequence 1321, App sequence 1339, App sequence 1339, App sequence 62, Appli sequence 62, Appli sequence 44, Appli sequence 44, Appli sequence 46, App sequence 47, Appli sequence 2075, Appli sequence 218, Appli sequence 254, Appli sequence 276, Appli sequence 51, Appli sequence 20276, Appli sequence 20276, Appli sequence 63, Appli sequence 40, Appli sequence 50, Appli sequence 40, Appli sequence 50, Appli seque
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GENERAL INFORMATION:

APPLICANT: Pia M. Challita-Eid

APPLICANT: Rene S. Hubert

APPLICANT: Rene S. Hubert

APPLICANT: Arthur B. Raitano

APPLICANT: Arthur B. Raitano

APPLICANT: Mary Faris

APPLICANT: Mary Faris

APPLICANT: May Jakobovits

APPLICANT: Aya Jakobovits

TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN

TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS

FILE REFERENCE: 129.34US01 (511582003400)

CURRENT APPLICATION NUMBER: US/09/799,250B

CURRENT FILING DATE: 2003-07-14

NUMBER OF SEQ ID NOS: 721

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapiens
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US-09-103-664A-2
US-08-973-462-8
US-08-272-255-16
PCT-US95-08565-16
US-10-164-595-64
US-09-914-259-64
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Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Scoring table: sequence: Title: Perfect score:

BLOSUM62

Gapop 10.0 , Gapext 0.5

US-10-087-190-3 1047

Run on:

OM protein - protein search, using sw model

Copyright

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APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
APPLICANT: Day Jakobovits
ITITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
ITITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
ITITLE ARFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 720
LENGTH: 198
TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
US-09-799-250B-720
                                                                                                                                                                                                                                                                                  APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Mary Faris
APPLICANT: May Jakobovite
TITLE OF INVENTION: 12191F1: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION UNMER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
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US-09-799-250B-4
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SEQ ID NO 4
IENGTH: 205
TYPE: PRT
ORGANISM: Mus musculus
                                                                    Query Match 90.5%; Score 948; DB 2; Length 205, Best Local Similarity 89.3%; Pred. No. 1.2e-84; Matches 183; Conservative 10; Mismatches 12; Indels
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Patent No.
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RESULT 5
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APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
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Patent No. 6639063
GENERAL INFORMATION:
TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCER
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: PASCEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 200
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SOFTWARE: Patent.pm
SEQ ID NO 4959
LENGTH: 127
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Best Local Similarity
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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
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CURRENT FILING DATE: 2000-07-21
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Pred. No. 2.4e-50;
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TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34USO1 (511582003400)
CURRENT APPLICATION UNWHERE: US/09/799,250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 721
LENGTH: 200
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Best Local 9
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GENERAL INFORMATION:
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APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitc
APPLICANT: Arthur B. Raitano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                         Match 33.3%; Score 349; DB 2; Length 200 Local Similarity 41.6%; Pred. No. 3.2e-26; es 84; Conservative 36; Mismatches 76; Indels
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                                                                                                                     181 KRKFGFEENKIDRTFGIPEDFD 202
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                                                                                                                                                                                                                                                                                                                         1 KGLSLAEKRRLEAIFHDSKDFFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK
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                                                                                                                                                                                                                                                                                   IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI--EKAKIGRCETE-ERT 121
                                                                                                                                                                                                                                                                                                                                                     KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64
                                                                                                                                                             QYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI--EKAKIGRCETE-ERT 121
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                                                                                -RDMGADTNQIREYCSIPEDLD 200
                                                                                                                                                                                                                                           IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN
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Steve Chappell Mitchell
Arthur B. Raitano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daniel E.H. Afar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mary Faris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
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                                                                                                                                                                                                                                             119
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Sequence 14485, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
ITITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO (
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
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                                                                                           US-09-538-092-1321
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                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version
SEQ ID NO 1321
LENGTH: 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14485
LENGTH: 260
    Matches
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1321, Application US/09538092 Patent No. 6753314
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Best Local Similarity 27.1%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
                                                                                                    NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q14203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 NRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDFDYI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 C--ETEERTRLAKELSSIR-----DQREQLKAEVEKYKDCDPQVVEBIRQANKVAKEAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 EQDRCGTTNLYWSFP-----YLQHKKQ------QETHDRLNRTIANLETERDSLICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAK-----IGR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 MPPKKGLTQEEKLSALLNWFQSDHMFYTLKEIESKASKQCKIPPMQMKELVLALVEEGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKDETGVRNQTHERASKIRFCDQSLERIDSIQSQLQSLKDSBS--VE---
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    Conservative
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12.8%; Score 134.5; DB 2; 23.4%; Pred. No. 0.00032; vative 43; Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Method
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                                              Length 1270;
       Indels
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    Gaps
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                                                                                                                                                                                            Matches
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 752-5958 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: LU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      LENGTH: 976 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/104,324B FILING DATE: 25-June-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 6232460man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                           ocal Similarity
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                                                             472 QAREKEVHDLEIQLTAITTSEQYYSKEVKDLKTELENEKLKNTELTSHCNKLSLENKELT
                                                                                                                            413 QKKSSELEEMTKLTNNKEVELEBLKKVLGEKETLLYBNKQFEKIAEELKG-TEQELIGLL
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                                                                                                                                                          3 KKKGLSAEE--KRTRMMEI-FSETKDV------FQLKDLEKIAPKEKGITAMSVKEVL 51
                                                                                                                                                                                            63;
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                                                                                             QSL---VDDGMVDCERIGTSNYYWAFPSKAL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALVRMRDLSSSEKQEHVKLQKLMEK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIGRCET--EERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANR 168
                               ------SQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREQ 136
QETSDMTLELKNQQEDINNNKKQEERMLKQIE--NLQETETQLRNELEYVREELKQKRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Fulbright & Jaworski LLP
666 Fifth Avenue
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                       (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ozlem; Sahin, Ugur; Pfreundschuh, Michael
Methods For Diagnosis And Treating Cancers,
And Methods For Identifying Pathogenic Markers In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 6232460mal Cells
                                                                                                                                                                                                         11.2*; Score 117; DB 2; Length 976; 23.9*; Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                  30,946
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                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 kb storage
                                                                                                                                                                                            85; Indels
                                                                                              ------HARKHKLEVLE--
                                                                                                                                                                                            78;
                                                                                                                                                                                          Gaps
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US-09-538-092-1339
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         Sequence 55, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
   CURRENT APPLICATION NUMBER: US/09/914,259
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Sequence 1339, Application Fatent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic APPLICANT: Mansfield, T
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PRIOR ON THE 1999-04-01
PRIOR PRICIATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
PRIOR PRICIATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1339
SEQ ID NO 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q15431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 11.2%; Score 117; DB 2; Length 976; Local Similarity 23.9%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 LESAKQKFGEITDTYQKEIEDKKI 673
                                                                                                                                                                                                                                                                                                                                                                                                                   413 OKKSSELEEMTKLTNNKEVELEELKKVLGEKETLLYENKQFEKIAEELKG-TEQELIGLL 471
                                                                                                                                                                                                                                                                                                                                                               52 QSL---VDDGMVDCERIGTSNYYWAFPSKAL-------HARKHKLEVLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KKKGLSAEE--KRTRMMEI-FSETKDV-----FQLKDLEKIAPKEKGITAMSVKEVL 51
                                                                                                                                                                                                        QETSDMTLELKNQQEDINNNKKQEERMLKQIE--NLQETETQLRNELEYVREELKQKRDE
                                                                                                                                                                                                                                                                                                               QAREKEVHDLEIQLTAITTSEQYYSKEVKDLKTELENEKLKNTELTSHCNKLSLENKELT 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SWAKRKFG-----FEENKI 191
                                                                                                    VKCKLDKSEENCNNLRKQVENKNKYIEELQQENKALKKKGTAESKQLNVYEIKVNKLELE 649
                                                                                                                                                    LKABVEKYKD-CD------PQVVBEIRQANKVAKB--AANRWTDNIFAIK-----
                                                                                                                                                                                                                                                           -----SQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREQ 136
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                                                      -SWAKRKFG-----FEENKI
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                                                      191
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GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 284
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-914-259-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO 55
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-914-259-55
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US-09-914-259-62
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RESULT 13
US-09-248-796A-20275
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                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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Local Similarity 23.2%;
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                                                                                                                                                161 KYEEVARKLVIIESDLERAEERAELSEGKC-----AELEEELKTVTNNLKSLEAQAEKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 SERGM-----KVIESRAQKDEEKMEIQEIQLKEA--KHIAEDADRKYE
                                                                        216 QKEDKYEEEIKVLSDKLKEAETR--
                                                                                                                                                                                                                          104 ---ERLATALQKLEBAEKAADESERGMKVIESRAQKDEEKMEIQEIQLKEAKHIAEDADR 160
                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ---GMVDCERIGTSNYYWAFPSKALHAR----KHKLEVLESQLSEGSQKH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 LAEKKATDAEADVASLNRRIQLFEEELDRAQ----ERLA-----TALQKLEEAEKAADE
                                                                                                                                                                                                                                                                                                                                                                          48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKKKGLSAE---EKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDD
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                                                                                                                                                                                                                                                                                                                                   2 SKKKGLSA-EEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVK-EVLQSLVDDGM 59
                                                                                                           DCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                                                                                                                                           VDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVARKLVIIESDLERAEERAELSEGKC----AELEEELKTVTNNLKSLEAQAEKYSQKE
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                                                                                                                                                                                                                                                                                              AKEKLLRASEDERDRVILEELHKAEDSLLAAD-ETAAKAEADVASLNRRIQLVEEELDRAQ 103
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                                                                                                                                                                   ---HASLQKSIEKAKI--GRCETEERTRLAKELSSLRDQREQLKAEVEKYK 145
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180
Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 113.5; DB 21.1%; Pred. No. 0.0048;
                                                                                                                                                                                                                                                                                                                                                                          48; Mismatches
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Pred. No. 0.0043;
                                                                          ----AEFAERSVTKLEKSID 254
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
VNUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20275
LENGTH: 630
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20275
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                                                                                                                                                                                                                                                       ; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-43
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US-09-914-259-43
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CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
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GENERAL INFORMATION:
                                                                                                                                                                   Query Match 10.7%; Score 112; DB 2; Best Local Similarity 23.5%; Pred. No. 0.0068; Matches 52; Conservative 41; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 49; Conservative 43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
  133 R----ALKDEEKMELQEI---
                                        48 KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DCERIGTSNYYWAFPS--KALHARKHKLEVL----ESQLSEGSQKHASLQKSI-----
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                                                                                                                         1 MSKKKGLSAEEK---RTRMMEIFSETKDVFQ-----LKDLEKIAPK-EKGITAMSV 47
                                                                                   LAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIEN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N---DN-----SGAKKELLEKVSKLE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTKNSDTELKLEKQLEELEKVK-----LDLQTADEKLKGITEREIALKSELETVKNSG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LSTTSELAALTKTVKSLEKEKEELQFLSGNKSKELEDYIQKHSDISEKLKALTDEL
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                                                                                                                                                                 41;
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  ----QLKEAKHIAEEADRKYEEVARKLVIIEGDL
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GENERAL INFORMATION: Glot, Loic
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/173,352
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 918
LENGTH: 1937
TYPE: PRT
ORGANISM: Homo mapiens
FEATURE: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P13535
US-09-538-092-918
Search completed: February
Job time : 48 secs
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US-09-538-092-918
; Sequence 918, Application US/09538092
; Patent No. 6753314
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                                                                                          1536 VEOEK-CEIOAALEBABASLEHBEGKILRIQLBLNOVKSEVDRKIABKDEBIDO 1588
                                                                                                                                                                                              1476 ESRSISTELFKVKNVYEESLDQLETLRRENKNIQQEISDLTEQIAEGGKQIHELEKIKKQ 1535
                                                                                                                                                                                                                                                                                             1421 KQRLQNEVEDLMLDVERSNAACAALDKKQRNF-----DKVLSEWKQKYEETQAELEASQK 1475
                                                                                                                                                                                                                                                                                                                                                                                               1361 QRALSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQEAEEHVEÄVNAKCASLEKT 1420
                                                                                                                                             141 VEKYKOCOPOVVEEIROANKVAKEA-ANRWIDNIFAIKSWAKRKFGFEENKIDR 193
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                                                                                                                                                                                                                                               99 KHASLQKSIEKAK-----IGRCET--EERTRLAKELSSLRDQ-----REQLKAE 140
                                                                                                                                                                                                                                                                                                                                              48 KEVLQSLVDDGMVDCERIGTS-----NYYWAFPSKALHARKHKLEVLESQLSEGSQ 98
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Sequence 3, Application US/10087190 Publication No. US20030223997A1
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

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Sequence 2, Application US/09799250
Publication No. US20030032087A1
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovita
APPLICANT: Aya Jakobovita
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-799-250-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-799-250-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 205
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; P
Matches 205; Conservative 0;
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TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
                                                                                                               121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
                                                                                                                                                                                                         61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
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                       KRKFGFEENKIDRTFGIPEDFDYID 205
                                                                                     TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA
KRKFGFEENKIDRTFGIPEDFDYID
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                                                                              APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF EGG ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pla M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: S1158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
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                  LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
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Afar, Daniel E. H.
Ge, Wangmao
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; Sequence 20, Application US/10087190
; Publication No. US20030223997A1
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Best Local Sim
Matches 205;
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APPLICANT: Challita-Eid, I
APPLICANT: Hubert, Rene S
APPLICANT: Raitano, Arthu
APPLICANT: Fails, Mary
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Best Local Similarity
Matches 205; Conserv
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APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
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                          KRKFGFEENKIDRTFGIPEDFDYID 205
                                                                                                      TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
                                                                                                                                                         DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
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Faris, Mary
Afar, Daniel E. H.
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                                                                             TRLAKELSSIRDQREQIKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA
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  KRKFGFEENKIDRTFGIPEDFDYID
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                                                                                                                                                                                                                                                                                                                100.0%; Score 1047; DB 4; ilarity 100.0%; Pred. No. 4e-78; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4e-78;
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US-10-087-190-21 ; Sequence 21, Application US/10087190

RESULT 5

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APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 9/779,250
PRIOR APPLICATION NUMBER: US 9/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
SEQ ID NO 22
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ORGANISM: Homo Sapiens US-10-087-190-22
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US-10-087-190-22
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US-10-087-190-21
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APPLICANT: Challita-Eid,
APPLICANT: Hubert, Rene
APPLICANT: Raitano, Arth
APPLICANT: Faris, Mary
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APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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LENGTH: 205
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
IIITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCES: 51158-20034-02
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT PILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
NUMBER OF SEQ ID NOS: 69
NUMBER OF SEQ ID NOS: 69
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
                                            LENGTH: 205
TYPE: PRT
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Local Similarity 100.0%;
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Afar, Daniel E. H.
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Afar, Daniel E. H.
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US-10-087-190-61
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                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 205; Conserv
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Best Local Similarity
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PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FRANCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEPUL IN TREATMENT AND DETECTION OF CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Agensys, Inc
APPLICANT: Challita-Eic
APPLICANT: Hubert, Rene
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 KRKFGFEENKIDRTFGIPEDFDYID 205
                     KRKFGFEENKIDRTFGIPEDFDYID 205
                                                                    TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA
                                                                                                                                      DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER
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Afar, Daniel E. H.
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Pred. No. 4e-78;
Mismatches
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RESULT 8 US-10-408-765A-1821

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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Fahy, Eoin D.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF 5EQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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US-11-125-805-2
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                                                            US-11-125-805-2
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LENGTH: 205
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20
GENERAL INFORMATION:
                                                                             SEQ ID NO 2
LENGTH: 205
TYPE: PRT
ORGANISM: Homo sapiens
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Query Match
Best Local Similarity
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TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129 34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/11/125,805
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/09/799,250B
PRIOR FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
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APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
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                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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Mary Faris
Daniel E.H. Afar
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100.0%;
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Pred. No. 4e-78;
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APPLICANT: Falls, Fight
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
ITITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
ITITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-44
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Best Local Similarity
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APPLICANT: Challita-Eid, Pia
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
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                AKRKFGFEENKIDRTFGIPEDFDYID 205
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ilarity 99.5%;
Conservative
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Pred. No. 3e-77;
0; Mismatches
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                                                                                                                                                                                                                                                                                                              206;
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RESULT 11
US-10-087-190-45
; Sequence 45, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:

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APPLICANT: Afar, Daniel E. H.

APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121PIF1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-45

COMMISM: SCORE 1036.5; DB 4; Length 206;
                                                                                              APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Hubbert, Rene S.
APPLICANT: Hubbert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: BATITLED 121PLF1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034-20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF ESG ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-087-190-24
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                                       US-10-087-190-24
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Query Match
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APPLICANT:
APPLICANT:
                                                     LENGTH: 198
TYPE: PRT
ORGANISM: Homo Sapiens
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APPLICANT: Challita-Eid, Pia M.
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Afar, Daniel E. H.
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   96.6%;
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Pred. No. 3e-77;
0; Mismatches
     Score 1011;
     DB
     4.
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   Length 198;
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   RESULT 14
US-10-687-190-13
; Sequence 13, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
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APPLICANT: Mary Faris
APPLICANT: Mary Faris
APPLICANT: Apa Jakobovits
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 12191F1: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/11/125,805
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/09/799,250B
PRIOR PILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 720
LEMETH: 198
TYPE: PRT
ORGANISM: Schizobaccharomyces pombe
US-11-125-805-720
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US-11-125-805-720
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APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitch
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel B.H. Afar
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Best Local Similarity 100.0%; Pred. No. 3.5e-75;
Matches 198; Conservative 0; Mismatches 0;
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Steve Chappell Mitchell
Arthur B. Raitano
GFEENKIDRTFGIPEDFD 198
                        GFEENKIDRTFGIPEDFD
                                                                                                           KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKF
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Mismatches 0;
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APPLICANT: Fails, Mary
APPLICANT: Afar, Daniel B. H.
APPLICANT: Ge, Mangmao,
APPLICANT: Jakobovitz, Aya
ITILE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANC
FILE REPERENCE: 51158-20034.20
FULE REPERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FRACESEQ for Windows Version 4.0
SEQ ID NO 13
                               ; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo S
US-10-087-190-19
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-087-190-19
                                                                                                 APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, P.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.
APPLICANT: Ge, Wangmao
APPLICANT: Gakobovitz, Aya
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/10087190 Publication No. US20030223997A1
Query Match
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APPLICANT:
APPLICANT:
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Challita-Eid, Pia M.
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Raitano, Arthur B.
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Afar, Daniel E. H.
Ge, Wangmao
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                                                   Sapiens
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93.1%; Score 975;
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BB
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Length 190;
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                                                                           136 QLKAEVEKYKDCDPQVVEEIRQANKVAKBAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
181 GIPEDFDYID 190
                             196 GIPEDFDYID 205
                                                                                                                                                 76
                                                                                                                                                                                                   16 MMBIFSBTKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCBRIGTSNYYWAFP
                                                                                                                    61 SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE 120
                                                                                                                                                                               1 MMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
                                                                                                                                     SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE 135
                                                         QLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 180
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Search completed: February 2, 2006, 12:56:14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO3_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO3_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO3_NEW_PUB.pep:*
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   US-11-155-288-20
US-11-019-711-59
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US-11-069-834-54
US-11-069-834-63
US-11-069-834-63
US-10-821-234-163
US-11-069-834-56
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US-11-069-834-59
US-11-059-561-600
US-10-995-561-600
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Sequence 20, Appl Sequence 59, Appl Sequence 31, Appl Sequence 214, App Sequence 215, App Sequence 215, App Sequence 44, App Sequence 1632, App Sequence 1632, App Sequence 56, Appl Sequence 56, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appl Sequence 10, Appli Sequence 1171, App Sequence 11
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VKCKLDKSEENCNNLRKQVENKNKYIBELQQENKALKKKGTAESKQLNVYBIKVNKLELE 649 QETSDMTLELKNQQEDINNNKKQEERMLKQIE--NLQETETQLRNELEYVREELKQKRDE 589 -----SQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREQ

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RESULT 2

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QKKSSELEEMTKLTNNKEVELEELKKVLGEKETLLYENKQFEKIAEBLKG-TEQELIGLL

QSL---VDDGMVDCERIGTSNYYWAFPSKAL------HARKHKLEVLE--QAREKEVHDLEIQLTAITTSEQYYSKEVKDLKTELENEKLKNTELTSHCNKLSLENKELT 531

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532

φ	Query M Best Lo Matches	CURRENT AP CURRENT FILI PRIOR APPL PRIOR FILI NUMBER OF SOPTWARE: SEQ ID NO 2 LENGTH: 9 TYPE: PRT ORGANISM: US-11-155-288	RESULT 1 US-11-155-288-20 ; Sequence 20, A ; Publication No ; GENERAL INFORM ; APPLICANT: Ch ; APPLICANT: Ch ; APPLICANT: CN ; APPLICANT: NO ; TITLE OF INVE ; TITLE OF INVE ; TITLE OF INVE		45	4 4 4 W	42	4 C	39	38 7	36	ա 4. ռ	33	υ u	30	28 29	27	26	
3 KKK	atch cal Simi 63;	CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2005-06-17 PRIOR APPLICATION NUMBER: 60/580 PRIOR FILING DATE: 2004-06-17 NUMBER OF SEQ ID NOS: 40 SOFTWARE: FastSEQ for Windows Ve EQ ID NO 20 LENGTH: 976 TYPE: PRT ORGANISM: Homo sapiens 11-155-288-20	-11-155-288-20 -11-155-288-20 Sequence 20, Application US/111 Publication No. US20060008468A1 REPULICANT: Chiang, Chih-Sheng APPLICANT: Simard, John J.L. TITLE OF INVENTION: COMBINATIO TITLE DEFENSELYE. MANNEY CSOA		84	8 4 4 4	84.5	84. 5	84.5	84.5	85	87.5 86	88	88	88	8 8	88	88.5	
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KRTRMMEI-	11.2 23.9 vative	NUMBER: U 2005-06 MBER: 60/ 004-06-17 : 40 r Windows	ttion US/11155 060008468A1 Chih-Sheng John J.L. COMBINATIONS ANTIGENS IN		1652	663	3116	2480	1641	693 448	227	1732	5464	5406	5335	3960	1299	1404	
- MEI	" 9 2 # #	06- 0/5 17	/111 58A1 eng .L. ATIC		9		יסנ												
- FSETKDVFQLKDLEKIAFKEKGITAMSVKEVL	Score 117; DB 7; Length 9 Pred. No. 0.094; 38; Mismatches 85; Indels	MBER: US/11/155,288 2005-06-17 ER: 60/580,969 /4-06-17 40 Windows Version 4.0	US/11155288 18468A1 Sheng J.L. JINATIONS OF TUMOR-ASSOCIATED INGENS IN DIAGNOSTICS FOR VARIOUS	ALIGNMENTS	US-10-995-561-663	US-11-196-475-78	US-10-995-561-826	US-10-995-561-825	US-10-877-346-40	US-10-873-528-185 US-10-793-626-1728	US-11-215-658-12	US-10-055-877-147	US-10-995-561-775	US-10-995-561-774	10-995-	US-10-995-561-771	10-821-234-	-10-878-556A-16	
NPKEKGITAMS	976; ls 78;		TYPES OF		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
SVKEVL	Gaps		CANCERS		663,		826,	825,	40,	1726	12,	147	775,	774,	777,	771,	1145,	169,	
51	13;		χ. G		App	App1	App	App	Appl	Ą p	Appl	App	App	App	App	App	ď	App	

US-11-019-711-59

GENERAL INFORMATION: Sequence 59, Appropriate No.

Application US/11019711 10. US20060009634A1

APPLICANT: Kekuda, Ramesh

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                                                                                                                                  ; OTHER INFORMATION: ; OTHER INFORMATION: US-11-019-711-59
                                                                                                                                                                                                                                                   SEQ ID NO 59
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APPLICANT:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-09-12 NUMBER OF SEQ ID NOS: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
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                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
                                                                                                                                                                                                                                 ENGTH: 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/260,018
FILING DATE: 2001-01-05
APPLICATION NUMBER: 60/260,360
FILING DATE: 2001-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/272,411
FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/318,700
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/318,405 FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-07-05
APPLICATION NUMBER: 60/305,060
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-05-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/272,817
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-07-1
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/303,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LING DATE:
                                   13
RKKHQDAINELSE--QIEQLQKQKAK-----AEKEKSQLQAEVDDLLAQLDSI-----
                                RTRMMBIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYW
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Padigaru, Muralidhara
Taupier Jr, Raymond J
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Boldog, Ferenc L
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Sciore, Paul
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Vernet, Corine A.M.
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Tchernev, Velizar T
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Malyankar, Uriel M
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                                                                                                                                                Description of Artificial Sequence: Mysosin Tail Consensus Sequence
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                                                                                 10.4%;
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                                                                Score 108.5;
Pred. No. 0.36
27; Mismatches
                                                                            .36;
                                                                                                DB 7;
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                                                                                                Length 860;
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RESULT 4
US-11-069-834-52
(US-11-069-834-52)
Sequence 52, Application US/11069834
; Publication No. US20050276811A1
; GENERAL IMPORMATION:
APPLICANT: CARROLL, MICHAEL C.
APPLICANT: HOORE JR., FRANCIS D.
APPLICANT: HECHTMAN, HERBERT B.
TITLE OF INVENTION: NATURAL ICM ANTIBODIES AND FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
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; TYPE: PRT
; ORGANISM: P.
US-11-196-400-3
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Best Local Similarity
Matches 47; Conserve
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CURRENT FILING DATE: 2005-08-04
PRIOR APPLICATION NUMBER: US/09/742,096
PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: US 08/973,462
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: PCT/FR96/00894
PRIOR FILING DATE: 1996-06-12
PRIOR APPLICATION NUMBER: FR 95/07007
PRIOR FILING DATE: 1995-06-13
PRIOR FILING DATE: 1995-06-13
NUMBER: OF SEQ ID NOS: 29
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SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 RQLEEAEAQVSNLSKLKSQLESQLEEAKRSLEE 254
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US-11-124-368A-214
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; TYPE: PRT
; ORGANISM: Mus musculus
US-11-069-834-52
                                                                                                                                                                                                                                         Best Loc
Matches
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APPLICANT: Michele Cargill
APPLICANT: James J. Devlir
APPLICANT: May Luke
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 214
LENGTH: 2665
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                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
-11-124-368A-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Genetic Polymorphisms Associated with TITLE OF INVENTION: Vascular Diseases, Methods of Detectifile Reference: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-9
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FASTSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 3.3
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                                                                          1794 RGIVSEKTÖKLSNMQKDLENSNAKLQEKIQELKANEHQLITLKKÖVNETQKKVSEMEQLK 1853
                                                                                                                                                         1737 IDKLRGIVSEKTNEISNMOKDLEHSNDALKAODLK--IQEELRIAHMHLKE-QQETIDKL
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                                                                                                                                                                                                                                                          Similarity
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  KQIKDQSLTLSKLEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLKESLQ 1913
                                       EKAK----IGRCETE----
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                                                                                                                 -----DGMVDCER-IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
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20.3%; Pred. No. 5.7;
ative 49; Mismatches
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24.7%; Pred. No. 4;
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                               ----ERTRLAKELSSIRDQREQLKAEVE 142
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US-11-069-834-54
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Publication No. US20050276811A1
GENERAL INFORMATION:
              SOFTWARE: PatentIn Ver.
SEQ ID NO 54
LENGTH: 1976
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                                                                               APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: HECHTMAN, HERBERT B.
TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF FILE REFERENCE: CRA-002.01
CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
PRIOR APPLICATION NUMBER: 60/588,648
PRIOR FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-03-01
NUMBER: OF SEQ ID NOS: 65
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
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TYPE: PRT
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Local Similarity 20.7%;
es 42; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKYKDCDPQVVEEIRQANKVAKE 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKQIKDQSLTLSKLEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLKESL 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGIVSEKTDKLSNMQKDLENSNAKLQEKVIQELKANEHQLITLKKDVNETQKKVSEMEQL 1856
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; Pred. No. 8.8;
47; Mismatches
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Sequence 994, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
PRIOR APPLICATION NOS: 1704
SOFTWARE: Pt SEQ Jenes Version 1.0
SEQ ID NO 994
LENGTH: 171
TYPE: PRT
ORGANISM: Homo sapiens
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US-11-069-834-48
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US-10-821-234-994
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US-11-069-834-54
                                                   Sequence 48, Application US/11069834
Publication No. US20050276811A1
GENERAL INFORMATION:
APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: HECHTMAN, HERBERT B.
APPLICANT: HECHTMAN, HERBERT B.
TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: CRA-002.01
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
              CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
PRIOR APPLICATION NUMBER: 60/588,648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          878 MERKHOOLLEEKNILAEOLOAETELFAEAEEMRARLAAKKO-----ELEEILHDLESRVE 932
                                                                                                                                                                                                                                                                                                                                   115 CETEERTRLAKELSSLRDQRE-QLKAEVEKYKDCDPQVVEEIRQANKVAKEAAN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.3%; l Similarity 23.6%; 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 9.2%; Score 96; DB 6. Similarity 20.7%; Pred. No. 0.49; 36; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                             KMAEE--KLTHKMEANKENREAQMAAKLERLREKDKH-IEEVRK-NKESKDPAD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFTMASSDIQVKELEKRASGQAFELILSPRSKESVPEFPLSPPKKKDLSLEEIQKKLEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  VDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGR 114
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Pred. No. 6.8;
37; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                              -RRKSHEAEVLKQLAEKREHEKEVLQKA I EENNNFS
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Best Local :
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                     154
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1632
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US-10-821-234-1632
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CURRENT FILING DATE: 2004-044-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1632
LENGTH: 284
TYPE- DATE:
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PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 48
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Publication No. US20050255114A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Labat, Ivan
APPLICANT: Stacke-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 821A
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                                                                                                                                                                                                                                                                                                                                                                           y Match 9.0%; Score 94; DB 6; Length 284;
Local Similarity 24.5%; Pred. No. 1.3;
nes 51; Conservative 30; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1540 QLEELEDELQATEDAKLRLEVNLQAMKAQFER
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                                                                                                                                                                            63 -- ERIGTSNYYWAFPSKALHARKHKLEVL-------ESQLSEGSQKHAS 102
                                                                                                                                                                                                                                59 MVDCERIGTSNYYWAFPSKALHAR----KHKLEVLESQLSEGSQKH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Conservative 37; Mismatches
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EIRQANKVAKEAANRWTDNIFAIKSWAK 181
                                                                                                                      -----ASLOKSIEKAKIGRCETEERTR-LAKELSSLRDOREQLKAEVEKYKDCDPQVVE 153
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                                                                             KLVILEGELERSEERAEV----AESRARQLEEELRTMDQALKSLMASEEEYSTKEDKYEE 223
                                                                                                                                                                                                                                                                           AQEKLEQAEKKATDAEADVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERG
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                                                                               US-11-069-834-58
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Matches
                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/588,648
PRIOR FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTMARE: PATENTIN Ver. 3.3
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/11069834 Publication No. US20050276811A1
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Query Match 8.7%; Score 91.5; 1
Best Local Similarity 24.7%; Pred. No. 20;
Matches 45; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: humangp/chrl-aahl5403
DATABASE ENTRY DATE: 2003-04-22
                                                                                                                                                                                                                                                                                                          APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: HECHTMAN, HERBERT B.
TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: CRA-002.01
CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
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CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
                                                                                                LENGTH: 1992
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 SLRDQREQ------LKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWIDNIFAIKS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEELDRAQERLATA--LQKLEEAEKAADESERGMKVIENR----ALKDEEKMELQEI---
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                                        DB 7; Length 1992;
61;
    Indels
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RESULT 14
US-10-878-556A-44
; Sequence 44, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/588,648 PRIOR FILING DATE: 2004-07-16
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CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CARROLL, MICHAEL C. APPLICANT: MOORE JR., FRANCIS I APPLICANT: HECHTMAN, HERBERT B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NATURAL IGM ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                       1502 REARALSITRALEEEQEAREELERQNRALRAELEALLSSKDDVGKNVHELERARKAAEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1408 LEAGEEARRRAAREAETL-----TQRLAEKTEAVERLERARRRLQQELDDATVD----
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                                                                                                                                                                                                                                                                                                  166 AN 167
                                                                                                                                                                                                                                                                                                                                                                             122 RLAKELS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GTSNYYWAFPSKALHARKHKLEVLESQLSEGSQ----KHASLQKSIEKAKIGRCETEERT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTSNYYWAFPSKALHARKHKLEVLESQLSEGSQ----KHASLQKSIEKAKIGRCETEERT 121
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24.7%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                    LGQQKQLLSTLEKKQRKFDQLLAEEKAAVLRAVEDRE--RIEAEGRE
                                                                                                                                                                                                                                                                                                                                                                             -----SLRDQREQLKAEVE---KYKDCDPQVVEEIRQANKVAKEA 165
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RESULT 15
US-11-69-834-60
US-11-699-834-60
; Sequence 60, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-834-60
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TYPE: PRT

; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw hum/lama_human
; DATABASE ENTRY DATE: 1986-07-21
US-10-878-556A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'SOFTWARE: PatentIn version SEQ ID NO 44
                                                                                                                                                                                                                                                                                 Query Match 8.7%; Score 91; DB 7; Length 1995; Best Local Similarity 23.9%; Pred. No. 22; Matches 43; Conservative 33; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.7%; Score 91; DB 6; Length 664; Best Local Similarity 24.5%; Pred. No. 5.9; Matches 45; Conservative 24; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: HECHTMAN, HERBERT B.
TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: CRA-002.01
CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/588,648 PRIOR FILING DATE: 2004-07-16
                                                                                          1459 LVST-----LEKKQRKFDQLL-----ABEKAAVLRAVEERE--RABABGRERE
1500 ARALSITRALEEEQEAREELERQNRALRAELEALLSSKODVGKSVHELERACRVAEQAAN 1559
                                                                                                                                                                                       1414 AAREAEALTQRLAEKTETVDRL------ERG-----RRRLQQELDDATMDLEQQRQ 1458
                                                124 AKELS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 EVEK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 ELEK 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 EKRTLEGELHDLRGQVAKLEAALGEAKKQLQDEMLRRVDAEN------RLQTMKEELD 205
                                                                                                                                        65 -IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 SVAKERARLQLELSKVREEFKELKARNTKKEGDLIAAQARLKDLEALLNSKEAALSTALS
                                                                                                                                                                                                                                     8 SAEEKRIRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER--- 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLR----DQREQLKA 139
                          ----SLRDQREQLKAEVE---KYKDCDPQVVEEIRQANKVAKEAAN 167
                                                                                                                                                                                                                                                                                   Indels 54;
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Search completed: February 2, 2006, 12:56:28

Job time : 9 secs